PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/856,451A**

DATE: 07/07/2004
TIME: 16:09:33

Input Set : **A:\X12553.ST25.txt**
Output Set: **N:\CRF4\07072004\I856451A.raw**

```
 3 <110> APPLICANT: Eli Lilly and Company
 5 <120> TITLE OF INVENTION: Erythropoietic Compounds
 7 <130> FILE REFERENCE: X-12553
 9 <140> CURRENT APPLICATION NUMBER: US 09/856,451A
10 <141> CURRENT FILING DATE: 2001-05-22
12 <150> PRIOR APPLICATION NUMBER: PCT/US99/27801
13 <151> PRIOR FILING DATE: 1999-11-23
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 168
21 <212> TYPE: PRT
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: synthetic construct
28 <220> FEATURE:
29 <221> NAME/KEY: MISC_FEATURE
30 <222> LOCATION: (1)..(1)
31 <223> OTHER INFORMATION: Xaa at position 1 is absent or Met;
33 <220> FEATURE:
34 <221> NAME/KEY: MISC_FEATURE
35 <222> LOCATION: (2)..(2)
36 <223> OTHER INFORMATION: Xaa at position 2 is absent or is Ala, Cys, Asp, Glu, Phe,
Gly,
37        His, Ile, Leu, Met, Asn, Gln, Arg, Ser, Thr, Val, Trp, or Tyr
39 <220> FEATURE:
40 <221> NAME/KEY: MISC_FEATURE
41 <222> LOCATION: (26)..(26)
42 <223> OTHER INFORMATION: Xaa at position 26 is Asn, Lys or Glu;
44 <220> FEATURE:
45 <221> NAME/KEY: MISC_FEATURE
46 <222> LOCATION: (40)..(40)
47 <223> OTHER INFORMATION: Xaa at position 40 is Asn, Lys or Glu;
49 <220> FEATURE:
50 <221> NAME/KEY: MISC_FEATURE
51 <222> LOCATION: (78)..(78)
52 <223> OTHER INFORMATION: Xaa at position 78 is Arg or Glu;
54 <220> FEATURE:
55 <221> NAME/KEY: MISC_FEATURE
56 <222> LOCATION: (85)..(85)
57 <223> OTHER INFORMATION: Xaa at position 85 is Asn, Lys or Glu;
59 <220> FEATURE:
60 <221> NAME/KEY: MISC_FEATURE
61 <222> LOCATION: (90)..(90)
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ENTERED

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```
 62 <223> OTHER INFORMATION: Xaa at position 90 is Trp, Lys, Pro, or Arg;
 64 <220> FEATURE:
 65 <221> NAME/KEY: MISC_FEATURE
 66 <222> LOCATION: (128)..(128)
 67 <223> OTHER INFORMATION: Xaa at position 128 is Ser, Thr, Lys or Glu;
 69 <220> FEATURE:
 70 <221> NAME/KEY: MISC_FEATURE
 71 <222> LOCATION: (141)..(141)
 72 <223> OTHER INFORMATION: Xaa at position 141 is Arg or Glu;
 74 <220> FEATURE:
 75 <221> NAME/KEY: MISC_FEATURE
 76 <222> LOCATION: (156)..(156)
 77 <223> OTHER INFORMATION: Xaa at position 156 is Lys or Glu; and
 79 <220> FEATURE:
 80 <221> NAME/KEY: MISC_FEATURE
 81 <222> LOCATION: (168)..(168)
 82 <223> OTHER INFORMATION: Xaa at position 168 is Arg, absent, or any other amino acid.
 84 <400> SEQUENCE: 1
W-->  86 Xaa Xaa Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg
      87 1               5                  10                  15
W-->  90 Tyr Leu Leu Glu Ala Lys Glu Ala Glu Xaa Ile Thr Thr Gly Cys Ala
      91            20                  25                  30
W-->  94 Glu His Cys Ser Leu Asn Glu Xaa Ile Thr Val Pro Asp Thr Lys Val
      95            35                  40                  45
      98 Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu
      99      50                  55                  60
W--> 102 Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Xaa Gly Gln
     103 65                  70                  75                  80
W--> 106 Ala Leu Leu Val Xaa Ser Ser Gln Pro Xaa Glu Pro Leu Gln Leu His
     107                 85                  90                  95
     110 Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg
     111            100                 105                 110
W--> 114 Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Xaa
     115            115                 120                 125
W--> 118 Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Xaa Lys Leu Phe
     119      130                 135                 140
W--> 122 Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Xaa Leu Tyr Thr Gly
     123 145                 150                 155                 160
W--> 126 Glu Ala Cys Arg Thr Gly Asp Xaa
     127                 165
     130 <210> SEQ ID NO: 2
     131 <211> LENGTH: 193
     132 <212> TYPE: PRT
     133 <213> ORGANISM: homo sapiens
     135 <400> SEQUENCE: 2
     137 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
     138 1               5                  10                  15
     141 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
     142            20                  25                  30
```

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```
145 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
146         35                  40                  45
149 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
150         50                  55                  60
153 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
154 65                  70                  75                  80
157 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
158             85                  90                  95
161 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
162             100                 105                 110
165 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
166             115                 120                 125
169 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
170         130                 135                 140
173 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
174 145                 150                 155                 160
177 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
178             165                 170                 175
181 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
182         180                 185                 190
185 Arg
189 <210> SEQ ID NO: 3
190 <211> LENGTH: 498
191 <212> TYPE: DNA
192 <213> ORGANISM: homo sapiens
194 <400> SEQUENCE: 3
195 gctccaccac gtcttatttg tgattctcgt gttcttgaac gttacctgct ggaagctaaa     60
197 gaagctgaaa acatcaccac cggttgcgct gaacactgct ccctgaacga aaacatcacc    120
199 gttccggaca ccaaagttaa cttctacgct tggaaacgta tggaagttgg tcagcaggct    180
201 gttgaagttt ggcagggtct ggctctgctg tccgaagctg ttctgcgtgg tcaggctctg    240
203 ctggttaact cctcccagcc gtgggaaccg ctgcagctgc acgttgacaa agctgtttcc    300
205 ggtctgcgtt ccctgaccac cctgctgcgt gctctgggtg ctcagaaaga agctatctcc    360
207 ccgccggacg ctgcttccgc tgctccgctg cgtaccatca ccgctgacac cttccgtaaa    420
209 ctgttccgtg tttactccaa cttcctgcgt ggtaaactga aactgtacac cggtgaagct    480
211 tgccgtaccg gtgactga                                                  498
214 <210> SEQ ID NO: 4
215 <211> LENGTH: 165
216 <212> TYPE: PRT
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: synthetic construct
222 <400> SEQUENCE: 4
224 Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
225 1                   5                   10                  15
228 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
229             20                  25                  30
232 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
233         35                  40                  45
236 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
```

```
237      50                      55                      60
240 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
241 65                      70                      75                      80
244 Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
245                     85                      90                      95
248 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
249                 100                     105                     110
252 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
253             115                     120                     125
256 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
257         130                     135                     140
260 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
261 145                     150                     155                     160
264 Cys Arg Thr Gly Asp
265                     165
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/07/2004
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1,2,26,40,78,85,90,128,141,156,168

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```
L:86 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:90 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16
L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:32
L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:64
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:80
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:112
L:118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:128
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:144
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:160
```